

1/7

-231	GCAGCGGCACGGCAGCAGCGGCAACAAGTGCCGGACTAGCAGAGCCAAGCCGGAGCAGTC	-172
-171	CCTGCCGCCGACACCGCCGGGCGCCCGTCCGGGGCGCCGCGCATGGAGCGTGAGCTGCG	-112
-111	GCGGTCGCCGGGGCTGAGCCGCGCGGAGCGCCGGGACGTGGATGTGGCCGCGATCTCCCG	-52
-51	CCCTTGCCCCCGCCCCGCCGAGCTGGAGCTGCTCCCGACAAGATATGAGAAATGAGTGT	8
-16	<u>M S V</u>	3
9	TGGACGTGGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTATTT	68
4	<u>G R R R I K L L G I L M M A N V F I Y F</u>	23
69	TATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGGGAAGTAATAAT	128
24	<u>I M E V S K S S S Q E K N G K G E V I I</u>	43
129	ACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGGAACCGAGAGCA	188
44	<u>P K E K F W K I S T P P E A Y W N R E Q</u>	63
189	AGAGAAGCTGAACCGGCAGTACAACCCCATCTGAGCATGCTGACCAACCAGACGGGGGA	248
64	<u>E K L N R Q Y N P I L S M L T N Q T G E</u>	83
249	GGCGGGCAGGCTCTCCAATATAAGCCATCTGAACCTACTGCGAACCTGACCTGAGGGTCAC	308
84	<u>A G R L S N I S H L N Y C E P D L R V T</u>	103
309	GTCGGTGGTTACGGGTTTTAAACAACCTGCCGGACAGATTTAAAGACTTTCTGCTGTATTT	368
104	<u>S V V T G F N N L P D R F K D F L L Y L</u>	123
369	GAGATGCCGCAATTATCTACTGCTTATAGATCAGCCGATAAGTGTGCAAAGAAACCTTT	428
124	<u>R C R N Y S L L I D Q P D K C A K K P F</u>	143
429	CTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAAGCAATCCGGGA	488
144	<u>L L L A I K S L T P H F A R R Q A I R E</u>	163
489	ATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAACGGTGGTGCGAGTCTTCCTGCTGGG	548
164	<u>S W G Q E S N A G N Q T V V R V F L L G</u>	183
549	CCAGACACCCCCAGAGGACAACCACCCCGACCTTTTCAGATATGCTGAAATTTGAGAGTGA	608
184	<u>Q T P P E D N H P D L S D M L K F E S E</u>	203

FIG.1A

2/7

609	GAAGC	850	AAGAC	870	ATTCT	890	TATGT	668
204	K H Q	D I L	M W N	Y R D	T F F	N L S	L K	223
669	GGAAG	910	TGCTG	930	TTTCT	950	CAGGT	728
224	E V L	F L R	W V S	T S C	P D T	E F V	F K	243
729	GGGCG	970	ATGAC	990	GATGT	1010	TTTGT	788
244	G D D	D V F	V N T	H H I	L N Y	L N S	L S	263
789	CAAGAC	1030	CAAAG	1050	ATCTC	1070	TTTCA	848
264	K T K	A K D	L F I	G D V	I H N	A G P	H R	283
849	GGATA	1090	AAGCT	1110	GTAAG	1130	TACTA	908
284	D K K	L K Y	Y I P	E V V	Y S G	L Y P	P Y	303
909	TGCAG	1150	GGGGG	1170	TTTCT	1190	ACTCC	968
304	A G G	G G F	L Y S	G H L	A L R	L Y H	I T	323
969	TGACC	1210	AGTCC	1230	ATCTC	1250	ATGAT	1028
324	D Q V	H L Y	P I D	D V Y	T G M	C L Q	K L	343
1029	CGGC	1270	CTCGT	1290	TCCAG	1310	AGAAA	1088
344	G L V	P E K	H K G	F R T	F D I	E E K	N K	363
1089	AAATA	1330	ACATC	1350	TGCTC	1370	TATGT	1148
364	N N I	C S Y	V D L	M L V	H S R	K P Q	E M	383
1149	GATTG	1390	ATTTG	1410	GCTCA	1430	TTTAA	1208
384	I D I	W S Q	L Q S	A H L	K C *			397
1209	CAAT	1450	TTTGC	1470	ATAGA	1490	ATGTT	1268
1269	AATTT	1510	CTATA	1530	TAAAC	1550	CATGA	1328
1329	AACCT	1570	TTCA	1590	TTTGG	1610	TACTC	1388
1389	GGAT	1630	GATAT	1650	GCGAT	1670	GATTG	1448
1449	TTGT	1690	ACCCT	1710	CTTAT	1730	CTGAA	1508

FIG.1B

3/7

1509	1750 GCCCTCTTCTATAATATTCCTACTTCCCATAATAATGACTGATTTATTTGTAATTCAGGT	1770	1790	1568
1569	1810 ATTTATAAACCTATTGGCTACAAAGACTTTTGTTAAACATTATCCAGTGGTTTTTCGTGAAA	1830	1850	1628
1629	1870 TGGAATTATGTTTATTTTTATGGGATTTGGGTAAATTTTAAATTGTCTAGAAAACGAAA	1890	1910	1688
1689	1930 TTTCAGTTGTCAGTTGTGGAATTCAGTTTTTCAATTGTGGAAATTTCTGCCACCCCAAC	1950	1970	1748
1749	1990 AGTATTTTTGTGTGTTAATTAATTTTGC AAAATGAGAATCATGGTGTGACACTCATCTAA	2010	2030	1808
1809	2050 TTTATCTTGTGTGATGTTATGGTCATAATAAGGAGAAAGAGGGTTTAATTTTTCTTGTA	2070	2090	1868
1869	2110 TTTGGTTTCCTGGTGGTATCATAGTGTAATTTTAGTATTTGAAAATCAGTGTGATTCCTT	2130	2150	1928
1929	2170 AATGGCCAACTGAAGATTGAATTGCCGCTAACCAACCATATCGTGTTAGTGAATTTTCAAT	2190	2210	1988
1989	2230 ATGGACCAGGAAGGCATATGTATTTTGAAC TTGAGTGAAAAGGTTGAAGTTACAGACTTT	2250	2270	2048
2049	2290 TGCATAGATGGTTTGTCAATTTAAAAATCCAGAA TTATTATTGCCATATTTTCACATGC	2310	2330	2108
2109	2350 TGCTTATACAAGATTATTATTGAGTAGTAACTGTTCCCTGTCTATGTAGAAGTGCCTGTG	2370	2390	2168
2169	2410 TTTTTATTTATTGTTCCAGATCAAAGACCAAAACATTTTCTTAAATATCTCTTATGTAAT	2430	2450	2228
2229	2470 ATTTTATTTGTATACAGTGTGTTGTGATGAAATATTTAACTAGAGCATGATATTTTAAATG	2490	2510	2288
2289	2530 TTAAGGTGTAACATATGTAAATAAAACTGTTATTTTGAATTTTAAAATTTGTTTTTTG	2550	2570	2348
2349	2590 GGGGTATGAACTACTAGAGTTTAAAAATCTGCCAAACTATTACTTATATGTACTATTGTG	2610	2630	2408
2409	2650 TAACATACTTTCTTGAAATATTTTGT TTATAGAATTGAAGGTTCTTATCAGATGGGATA	2670	2690	2468
2469	2710 CTGGGGATTATAAACAATGGAAATAAAGCCACTGTATTTTAAAA	2730		2513

FIG. 1C

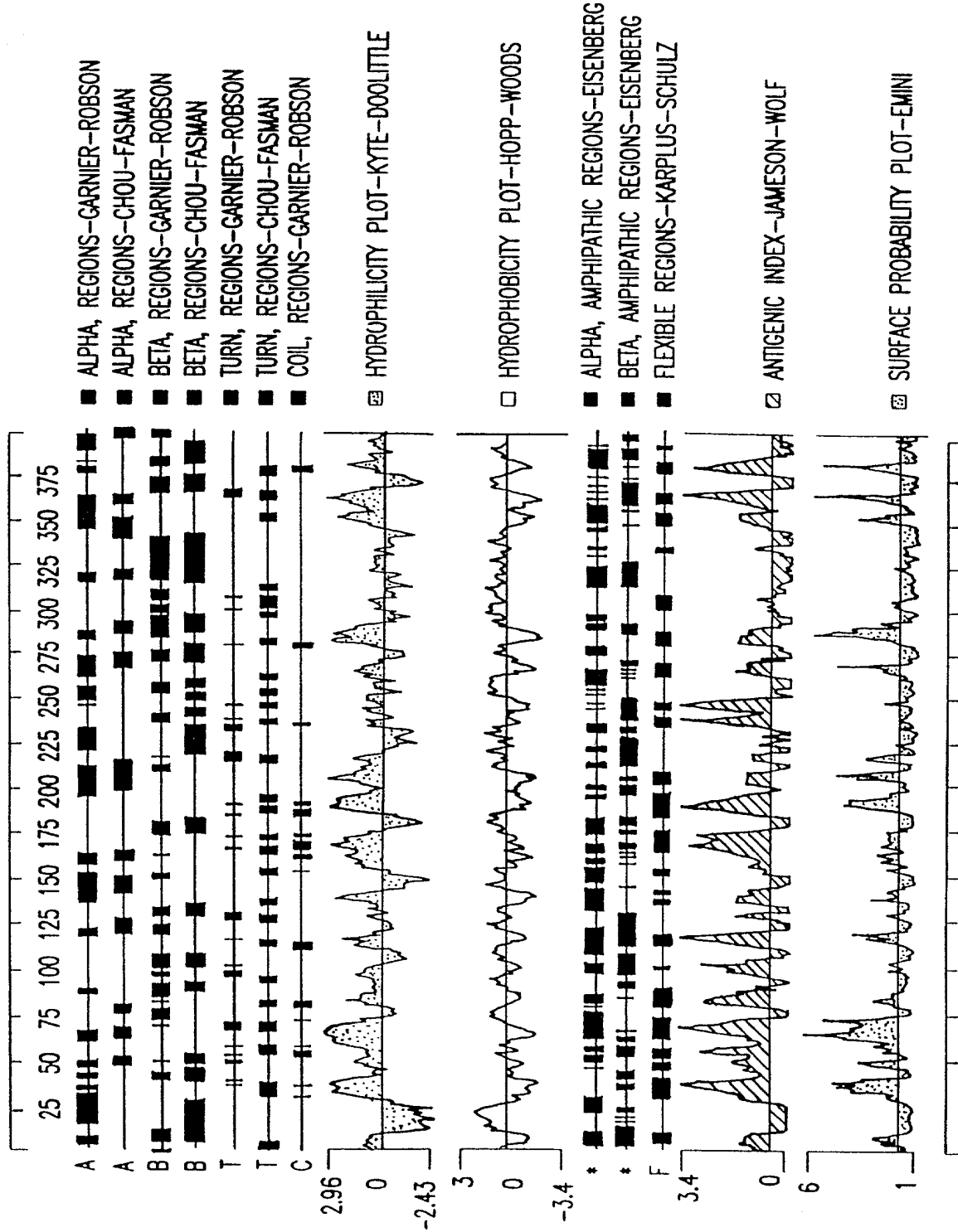
4/7

60	NREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGF	109
2	QSKHRKLLLRCLLVLPIL.LVDYCGLLTHLHLENF.ERHFHYPLNDDTG	49
110	NNLPDRFKDFLLYLRCRNYS..LLIDQPDKCAKKPFLLLAIKSLTPHFAR	157
50	SGSASSGLDKFAYLRVPSFTAEPVDPQPAR.....LTMLIKSAVGNSRR	93
158	RQAIRESWGQESNAGNQTVVRFLLGQTPPEDNHPDLSMDLKFESEKHQD	207
94	REAIRRTWGYEGRFSDVHLRRVFLGTAEDSEK.....VAWESREHGD	137
208	ILMWNYRDTFFNLSLKEVLFLRWVSTSCPDETFVFKGDDDFVNTHHILN	257
138	ILQADFTDAYFNNTLKTMLGMRWASEQFNRSEFYLFVDDYYVSAKNVLK	187
258	YLNLSLSTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYS.GLYPPYAGG	306
188	FLGRGRQSHQPELLFAGHVFQTSPLRHKFSKWYVSLEEYPFDRWPPYVTA	237
307	GGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRTF	356
238	GAFILSQKALRQLYAASVHLPLFRFDDVYLGIVALKAGISLQHCDDFRFH	287
357	DIEEKNNKNICSYYDLMLVHSRKPQEMIDIWSQLQSAHL	395
288	RPAYKGPDSYSSVIA..SHEFGDPEEMTRVWNECRSANY	324

FIG.2

5/7

FIG.3



6/7

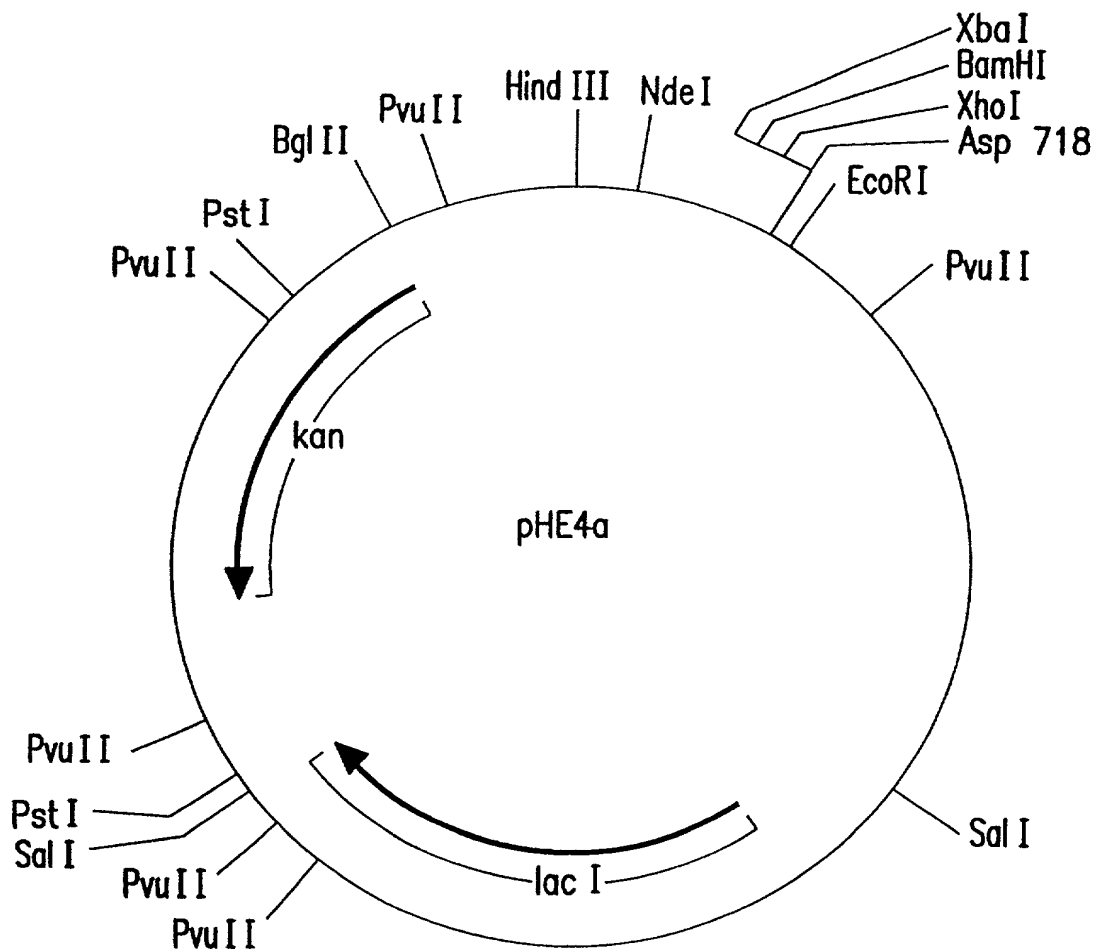


FIG.4

Appl. No. To be assigned; Group Art Unit: To be assigned
 Dkt. No. 1488.0620002/EKS/GLL;
 Inventors: SOPPET *et al.*; Tel: 202/371-2600
 Title: Cardiac and Pancreatic Protein and Gene

7/7

1 AAGCTT AAAAAGTGC AAAAATAGT TTTGAC TTTGAGCGGATAACAAT
 -35 Operator 1
 -10 Operator 2
 50 TAAGATGTACCCAAATTGAGCGGATAACAATTTCACACATTAA
 S/D
 94 ACAGGAGAAATTA CATATG

FIG.5